



## SEQUENCE LISTING

RECEIVED

MAY 16 2002

TECH CENTER 1600/2900

&lt;110&gt; PRODIGENE, INC.

&lt;120&gt; COMMERCIAL PRODUCTION OF LACCASE IN PLANTS

&lt;130&gt; 1015

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; 60/103,301

&lt;151&gt; 1998-10-05

&lt;160&gt; 3

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 1500

&lt;212&gt; DNA

&lt;213&gt; Trametes versicolor

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1497)

&lt;400&gt; 1

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ccc gac ggc ttc ctt cgg gat gcc atc gtg gtc aac ggc gtg gtc cct	96
Pro Asp Gly Phe Leu Arg Asp Ala Ile Val Val Asn Gly Val Val Pro	
20 25 30	
tcc ccg ctc atc acc ggg aag aag gga gac cgc ttc cag ctc aac gtc	144
Ser Pro Leu Ile Thr Gly Lys Lys Gly Asp Arg Phe Gln Leu Asn Val	
35 40 45	
gtc gac acc ttg acc aac cac agc atg ctc aag tcc act agt atc cac	192
Val Asp Thr Leu Thr Asn His Ser Met Leu Lys Ser Thr Ser Ile His	
50 55 60	
tgg cac ggc ttc ttc cag gca ggc acc aac tgg gca gac gga ccc gcg	240
Trp His Gly Phe Phe Gln Ala Gly Thr Asn Trp Ala Asp Gly Pro Ala	
65 70 75 80	
ttc gtc aac cag tgc cct att gct tcc ggg cat tca ttt ctg tac gac	288
Phe Val Asn Gln Cys Pro Ile Ala Ser Gly His Ser Phe Leu Tyr Asp	
85 90 95	
ttc cat gtg ccc gac cag gca gga acg ttc tgg tac cac agt cat ctg	336
Phe His Val Pro Asp Gln Ala Gly Thr Phe Trp Tyr His Ser His Leu	
100 105 110	
tct acg caa tac tgt gac ggg ctg cga gga ccg ttc gtc gtg tac gac	384

Ser Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro Phe Val Val Tyr Asp	
115 120 125	
ccc aag gat ccg cac gcc agc cgc tac gat gtt gac aac gag agc acg	432
Pro Lys Asp Pro His Ala Ser Arg Tyr Asp Val Asp Asn Glu Ser Thr	
130 135 140	
gtc atc acg ttg acc gac tgg tac cac acc gct gcc cgg ctc ggt ccc	480
Val Ile Thr Leu Thr Asp Trp Tyr His Thr Ala Ala Arg Leu Gly Pro	
145 150 155 160	
agg ttc cca ctc ggc gcg gac gcc acg ctc atc aat ggt ctt ggg cgg	528
Arg Phe Pro Leu Gly Ala Asp Ala Thr Leu Ile Asn Gly Leu Gly Arg	
165 170 175	
tcg gcc tcc act ccc acc gcc gcg ctt gct gtg atc aac gtc cag cac	576
Ser Ala Ser Thr Pro Thr Ala Ala Leu Ala Val Ile Asn Val Gln His	
180 185 190	
gga aag cgc tac cgc ttc cgt ctc gtt tcg atc tcg tgc gac ccg aac	624
Gly Lys Arg Tyr Arg Phe Arg Leu Val Ser Ile Ser Cys Asp Pro Asn	
195 200 205	
tac acg ttc agc atc gac ggg cac aat ctg acc gtc atc gag gtc gac	672
Tyr Thr Phe Ser Ile Asp Gly His Asn Leu Thr Val Ile Glu Val Asp	
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ggg atc aac agc cag cct ctc ctt gtc gac tct atc cag atc ttc gcc	720
Gly Ile Asn Ser Gln Pro Leu Leu Val Asp Ser Ile Gln Ile Phe Ala	
225 230 235 240	
gcg cag cgc tac tcc ttt gtg ttg aat gcg aac caa acg gtc ggc aac	768
Ala Gln Arg Tyr Ser Phe Val Leu Asn Ala Asn Gln Thr Val Gly Asn	
245 250 255	
tac tgg gtc cgc gcg aac ccg aac ttc gga acg gtt ggg ttc gcc ggg	816
Tyr Trp Val Arg Ala Asn Pro Asn Phe Gly Thr Val Gly Phe Ala Gly	
260 265 270	
ggg atc aac tcc gcc atc ctg cgc tac caa ggc gca cca gtc gcc gag	864
Gly Ile Asn Ser Ala Ile Leu Arg Tyr Gln Gly Ala Pro Val Ala Glu	
275 280 285	
ccc act acg acc cag acg acg tcg gtg atc ccg ctt atc gag acg aac	912
Pro Thr Thr Thr Gln Thr Thr Ser Val Ile Pro Leu Ile Glu Thr Asn	
290 295 300	
ttg cac ccc ctc gct cgc atg cct gtg cct ggc agc ccg aca ccc ggg	960
Leu His Pro Leu Ala Arg Met Pro Val Pro Gly Ser Pro Thr Pro Gly	
305 310 315 320	
ggc gtc gac aag gcg ctc aac ctc gcg ttt aac ttc aac ggc acc aac	1008
Gly Val Asp Lys Ala Leu Asn Leu Ala Phe Asn Phe Asn Gly Thr Asn	
325 330 335	
ttc ttc atc aac aac gcg act ttc acg ccg ccg acc gtc ccg gta ctc	1056
Phe Phe Ile Asn Asn Ala Thr Phe Thr Pro Pro Thr Val Pro Val Leu	

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Leu Gln Ile Leu Ser Gly Ala Gln Thr Ala Gln Asp Leu Leu Pro Ala			
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ggc tct gtc tac ccg ctc ccg gcc cac tcc acc atc gag atc acg ctg			1152
Gly Ser Val Tyr Pro Leu Pro Ala His Ser Thr Ile Glu Ile Thr Leu			
370	375	380	
ccc gcg acc gcc ttg gcc ccg ggt gca ccg cac ccc ttc cac ctg cac			1200
Pro Ala Thr Ala Leu Ala Pro Gly Ala Pro His Pro Phe His Leu His			
385	390	395	400
ggt cac gcc ttc gcg gtc gtt cgc agc gcg ggg agc acc acg tat aac			1248
Gly His Ala Phe Ala Val Val Arg Ser Ala Gly Ser Thr Thr Tyr Asn			
405	410	415	
tac aac gac ccg atc ttc cgc gac gtc gtg agc acg ggc acg ccc gcc			1296
Tyr Asn Asp Pro Ile Phe Arg Asp Val Val Ser Thr Gly Thr Pro Ala			
420	425	430	
gcg ggc gac aac gtc acg atc cgc ttc cag acg gac aac ccc ggg ccg			1344
Ala Gly Asp Asn Val Thr Ile Arg Phe Gln Thr Asp Asn Pro Gly Pro			
435	440	445	
tgg ttc ctc cac tgc cac atc gac ttc cac ctc gac gcg ggc ttc gcg			1392
Trp Phe Leu His Cys His Ile Asp Phe His Leu Asp Ala Gly Phe Ala			
450	455	460	
atc gtg ttc gca gag gac gtt gcg gac gtg aag gcg gcg aac ccg gtt			1440
Ile Val Phe Ala Glu Asp Val Ala Asp Val Lys Ala Ala Asn Pro Val			
465	470	475	480
ccg aag gcg tgg tgc gac ctg tgc ccg atc tac gac ggg ctg agc gag			1488
Pro Lys Ala Trp Ser Asp Leu Cys Pro Ile Tyr Asp Gly Leu Ser Glu			
485	490	495	
gct aac cag tga			1500
Ala Asn Gln			

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 <211> 499  
 <212> PRT  
 <213> Trametes versicolor

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 Pro Asp Gly Phe Leu Arg Asp Ala Ile Val Val Asn Gly Val Val Pro  
 20 25 30  
 Ser Pro Leu Ile Thr Gly Lys Lys Gly Asp Arg Phe Gln Leu Asn Val  
 35 40 45

Val	Asp	Thr	Leu	Thr	Asn	His	Ser	Met	Leu	Lys	Ser	Thr	Ser	Ile	His	50	55	60	
Trp	His	Gly	Phe	Phe	Gln	Ala	Gly	Thr	Asn	Trp	Ala	Asp	Gly	Pro	Ala	65	70	75	80
Phe	Val	Asn	Gln	Cys	Pro	Ile	Ala	Ser	Gly	His	Ser	Phe	Leu	Tyr	Asp	85	90	95	
Phe	His	Val	Pro	Asp	Gln	Ala	Gly	Thr	Phe	Trp	Tyr	His	Ser	His	Leu	100	105	110	
Ser	Thr	Gln	Tyr	Cys	Asp	Gly	Leu	Arg	Gly	Pro	Phe	Val	Val	Tyr	Asp	115	120	125	
Pro	Lys	Asp	Pro	His	Ala	Ser	Arg	Tyr	Asp	Val	Asp	Asn	Glu	Ser	Thr	130	135	140	
Val	Ile	Thr	Leu	Thr	Asp	Trp	Tyr	His	Thr	Ala	Ala	Arg	Leu	Gly	Pro	145	150	155	160
Arg	Phe	Pro	Leu	Gly	Ala	Asp	Ala	Thr	Leu	Ile	Asn	Gly	Leu	Gly	Arg	165	170	175	
Ser	Ala	Ser	Thr	Pro	Thr	Ala	Ala	Leu	Ala	Val	Ile	Asn	Val	Gln	His	180	185	190	
Gly	Lys	Arg	Tyr	Arg	Phe	Arg	Leu	Val	Ser	Ile	Ser	Cys	Asp	Pro	Asn	195	200	205	
Tyr	Thr	Phe	Ser	Ile	Asp	Gly	His	Asn	Leu	Thr	Val	Ile	Glu	Val	Asp	210	215	220	
Gly	Ile	Asn	Ser	Gln	Pro	Leu	Leu	Val	Asp	Ser	Ile	Gln	Ile	Phe	Ala	225	230	235	240
Ala	Gln	Arg	Tyr	Ser	Phe	Val	Leu	Asn	Ala	Asn	Gln	Thr	Val	Gly	Asn	245	250	255	
Tyr	Trp	Val	Arg	Ala	Asn	Pro	Asn	Phe	Gly	Thr	Val	Gly	Phe	Ala	Gly	260	265	270	
Gly	Ile	Asn	Ser	Ala	Ile	Leu	Arg	Tyr	Gln	Gly	Ala	Pro	Val	Ala	Glu	275	280	285	
Pro	Thr	Thr	Thr	Gln	Thr	Thr	Ser	Val	Ile	Pro	Leu	Ile	Glu	Thr	Asn	290	295	300	
Leu	His	Pro	Leu	Ala	Arg	Met	Pro	Val	Pro	Gly	Ser	Pro	Thr	Pro	Gly	305	310	315	320
Gly	Val	Asp	Lys	Ala	Leu	Asn	Leu	Ala	Phe	Asn	Phe	Asn	Gly	Thr	Asn	325	330	335	
Phe	Phe	Ile	Asn	Asn	Ala	Thr	Phe	Thr	Pro	Pro	Thr	Val	Pro	Val	Leu	340	345	350	

Leu Gln Ile Leu Ser Gly Ala Gln Thr Ala Gln Asp Leu Leu Pro Ala  
 355 360 365

Gly Ser Val Tyr Pro Leu Pro Ala His Ser Thr Ile Glu Ile Thr Leu  
 370 375 380

Pro Ala Thr Ala Leu Ala Pro Gly Ala Pro His Pro Phe His Leu His  
 385 390 395 400

Gly His Ala Phe Ala Val Val Arg Ser Ala Gly Ser Thr Thr Tyr Asn  
 405 410 415

Tyr Asn Asp Pro Ile Phe Arg Asp Val Val Ser Thr Gly Thr Pro Ala  
 420 425 430

Ala Gly Asp Asn Val Thr Ile Arg Phe Gln Thr Asp Asn Pro Gly Pro  
 435 440 445

Trp Phe Leu His Cys His Ile Asp Phe His Leu Asp Ala Gly Phe Ala  
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Ala Asn Gln

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 <212> DNA  
 <213> Zea mays

<220>  
 <223> Globulin-1 promoter

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 acaattacat atttacaaaa atgttttcta taaatattag atttagttcg tttatttgaa 180  
 tttcttcgga aaattcacat ttaaactgca agtcactcga aacatggaaa accgtgcatg 240  
 caaaataaat gatatgcatg ttatctagca caagttacga ccgatttcag aagcagacca 300  
 gaatcttcaa gcaccatgct cactaaacat gaccgtgaac ttgttatcta gttgtttaaa 360  
 aattgtataa aacacaaata aagtcagaaa ttaatgaaac ttgtccacat gtcatgatat 420  
 catatataga ggttgtgata aaaatttgat aatgtttcgg taaagttgtg acgtactatg 480  
 tgtagaaacc taagtgcact acacataaaa tcatagagtt tcaatgtagt tcactcgaca 540

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ggctttgaca ctcggaagcg cgctcgattc cagtagtgac agtaatttgc atcaaaaaata 720  
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ttctgcatac agccaacca a 1401